HIV-1 CTL Epitopes

How to Use Part I, the CTL Section

Section 1: HIV CTL Epitope Tables, Maps, and Alignments by Protein

This section summarizes HIV CTL epitopes arranged sequentially according to the location of the proteins in the HIV-1 genome. We attempted to make this section as comprehensive as possible, requiring that the epitope be contained within a defined region of 3 maximum of 30 amino acids, but not that the precise boundaries be defined. For more recent updates and useful searching capabilities, please see our Web site: `http://hiv-web.lanl.gov/immuno`

TABLES: each CTL reference has a six part basic entry:

- **Location:** The amino acid positions of the epitope boundaries and the reference sequence are listed as given in the primary publication. Frequently, these positions as published are imprecise, and do not truly correspond to the numbering of the sequence, but they provide a reasonable guide to the peptide's approximate location in the protein. Also, in many cases the reference sequence identification was not provided. Epitopes that cannot be approximated through peptide binding or interference are labeled disc for discontinuous.

- **WEAU Location:** The viral strain WEAU is used as a reference strain throughout this publication. The position of the defined epitope location on the sequence of the WEAU protein is indicated; obviously WEAU may not be identical to a given defined reactive sequence, so we simply indicating the aligned positions. The WEAU numbering corresponds to the protein maps in this database.

- **Epitope:** The amino acid sequence of the epitope of interest as defined in the reference, based on the reference strain used in the study defining the epitope. On rare occasions, when only the epitope location and not the actual epitope sequence was specified in the original publication, and the sequences were numbered inaccurately by the primary authors, we may have misrepresented the epitope's amino acid sequence. Therefore epitopes that were not explicitly written out in the text in the primary publication, that we determined by our looking up the reference strain and the numbered location, are followed by a question mark in the table.

- **Antigen:** The antigen that stimulated the CTL response.

- **Species(HLA):** The species responding and HLA specificity of the epitope.

- **Reference:** The primary reference.

  Following each entry for a given CTL epitope is a brief comment explaining the context of the study that defined the epitope.

MAPS:
The location and HLA restriction elements of CTL epitopes are indicated on protein sequences of the WEAU clone 1.60. This map is meant to provide the relative location of epitopes on a given protein, but the WEAU sequence may not actually carry the epitope of interest, as it may vary relative to the sequence for which the epitope was defined. Epitope regions are numbered, and the numbering on this map is used for the corresponding the epitope sequence alignments.
WEAU was chosen as the reference clone because it is one of the best characterized sequences currently available. The sequence was graciously provided prior to publication by George Shaw, and the manuscript describing the clone and sequence is in preparation. The clone was obtained from a

co-culture of this patient's PBMC's, first with normal donor PHA-stimulated lymphocytes for 14 days, and then with the H9 T-cell line for another 14 days. The blood specimen was obtained 15 days after the onset of clinical symptoms of acute (primary) infection, and 35 days after a single sexual encounter (receptive anal intercourse) with a partner whose virus was proven phylogenetically to be responsible for the transmission event. The single nucleotide deletion in nef in the WEAU 1.60 clone is NOT present in the patient's uncultured PBMCs where instead there is a "T." Thus, in the clone WEAU 1.60 nef is disrupted, but in the patient, the virus contains an intact nef gene in 10 out of 10 clones analyzed by PCR sequencing. The patient from whom WEAU 1.60 was derived is identified as "Patient #1" in *N Engl J Med* **324**:954–960, 1991 and as "WEAU 0575" in *Science* **259**:1749–1754, 1993. WEAU 1.60 and the virus isolate from which it was derived are SI (syncytium-inducing) strains. The full-length WEAU 1.60 provirus has been sequenced in its entirety by two different laboratories (G. Shaw and L. Hood) with 100% concordance.

ALIGNMENTS:
For each numbered epitope in the epitope-location protein maps, an alignment was generated from the protein sequence alignments in the HIV-1 genetic sequence database. All epitopes are aligned to the subtype B consensus (the most common amino acid found in subtype B in each position), with the sequence used to defined the epitope indicated directly beneath the B consensus. We used the 1996 HIV-1 database alignments for this section. The sequence database alignments were modified if there were multiple insertions made to maintain the alignment across the epitope, in an attempt to optimize the alignment across the epitope and minimize insertions and deletions. A dash indicates identity, and a period indicates an insertion made to maintain the alignment. Epitopes with stop codons are indicated with a $, and frameshifts a %; some epitopes carry only partial sequence.

Section 2: Table of HIV CTL Epitopes Sorted by HLA Restricting Elements

This section is a table of the epitopes included in Section 1 that have known HLA restricting elements, sorted by the restricting element. Anchor and auxiliary residues for HLA molecules are listed, and if anchor residues with appropriate spacing are evident in the epitope, they are emboldened and underlined. This table provides minimal information about the epitopes; for more information see the tables where epitopes are organized by location.

Section 3: References and notes.